

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Needleman, Philip  
Glenn, Kevin  
Krul, Elaine  
Gamson, Edward P.
- (ii) TITLE OF INVENTION: An Immunological Process and Constructs  
for Increasing the HDL Cholesterol Concentration
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Welsh & Katz, Ltd.
  - (B) STREET: 120 South Riverside Plaza, 22nd Floor
  - (C) CITY: Chicago
  - (D) STATE: IL
  - (E) COUNTRY: USA
  - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Gamson, Edward P.
  - (B) REGISTRATION NUMBER: 29,381
  - (C) REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (312)655-1500
  - (B) TELEFAX: (312)655-1501

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1431 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (viii) POSITION IN GENOME:
  - (C) UNITS: bp
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Drayna, Dennis  
Jarnagin, Alisha Stephens  
McLean, John  
Henzel, William  
Kohr, William  
Fielding, Christopher  
Lawn, Richard
  - (B) TITLE: Cloning and sequencing of human cholesteryl  
ester transfer protein cDNA
  - (C) JOURNAL: Nature

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(2) INFORMATION FOR SEQ ID NO:2:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln  
1 5 10 15

Val Ala Val His  
20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val  
1 5 10 15

Ala Tyr Arg Phe  
20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp  
1 5 10 15

Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu  
1 5 10 15

Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:6:

(ii) MOLECULE TYPE: peptide

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln  
1 5 10 15  
Leu Phe Thr Asn  
20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu Gly Arg Val Lys Tyr  
1 5 10 15  
Gly Leu His Asn  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
1 5 10 15  
Val Thr Val His  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val	Met	Val	Lys	Phe	Leu	Phe	Pro	Arg	Pro	Asp	Gln	Gln	His	Ser	Val
1				5					10					15	
Ala Tyr Thr Phe															
20															

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro	Glu	His	Leu	Leu	Val	Asp
1				5					10					15	
Phe Leu Gln Ser Leu Ser															
20															

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr	Thr	Val	Gln	Ala	Ser	Tyr	Ser	Lys	Lys	Lys	Leu	Phe	Leu	Ser	Leu
1				5					10					15	
Leu Asp Phe Gln															
20															

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu	Leu	Leu	His	Leu	Gln	Gly	Glu	Arg	Glu	Pro	Gly	Trp	Ile	Lys	Gln
1				5					10					15	

Leu Phe Thr Asn  
20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
1 5 10 15

Gly Leu His Asn  
20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGGAAATCT TCCAGGAGCT TTCCAGAGGC CTTCCACCG GCCAGGCCCA GGTAGCCGTC 60  
CAC 63

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGCCGTGA CGTTCGCTT CCCCCGCCCA GATGGCCGAG AAGCTGTGGC CTACAGGTTT 60

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

(2) INFORMATION FOR SEO ID NO:17:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

(2) INFORMATION FOR SEQ ID NO:18:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

(2) INFORMATION FOR SEQ ID NO:19:

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACGTCAGCG GCGAGAGGGC CGTGATGCTC CTCGGCCGGG TCAAGTACGG GCTGCACAAC 60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGAAATCT TCCAAGAGGT TGTCGGCGGC TTCCCCAGCC AGGCCCAAGT CACCGTCCAC 60

TGC 63

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGATGGTGA AATTCCTCTT TCCACGCCCA GACCAGCAAC ATTCTGTAGC TTACACATTT 60

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:  
(C) UNITS: bp

66

60

60

60

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 497 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (x) PUBLICATION INFORMATION:  
 (A) AUTHORS: Nagashima, M.  
 McLean, J. W.  
 Lawn, R. M.  
 (B) TITLE: Cloning and mRNA tissue distribution of  
 rabbit cholesteryl ester transfer protein  
 (C) JOURNAL: J. Lipid Res.  
 (D) VOLUME: 29  
 (F) PAGES: 1643-1649  
 (G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Cys	Pro	Lys	Gly	Ala	Ser	Tyr	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile	1	5	10	15
Thr	Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val	20	25	30	
Gln	Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg	35	40	45	
Ala	Val	Met	Leu	Leu	Gly	Arg	Val	Lys	Tyr	Gly	Leu	His	Asn	Leu	Gln	50	55	60	
Ile	Ser	His	Leu	Ser	Ile	Ala	Ser	Ser	Gln	Val	Glu	Leu	Val	Asp	Ala	65	70	75	80
Lys	Thr	Ile	Asp	Val	Ala	Ile	Gln	Asn	Val	Ser	Val	Val	Phe	Lys	Gly	85	90	95	
Thr	Leu	Asn	Tyr	Ser	Tyr	Thr	Ser	Ala	Trp	Gly	Leu	Gly	Ile	Asn	Gln	100	105	110	
Ser	Val	Asp	Phe	Glu	Ile	Asp	Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	115	120	125	
Glu	Leu	Thr	Cys	Asp	Ala	Gly	Ser	Val	Arg	Thr	Asn	Ala	Pro	Asp	Cys	130	135	140	
Tyr	Leu	Ala	Phe	His	Lys	Leu	Leu	Leu	His	Leu	Gln	Gly	Glu	Arg	Glu	145	150	155	160
Pro	Gly	Trp	Leu	Lys	Gln	Leu	Phe	Thr	Asn	Phe	Ile	Ser	Phe	Thr	Leu	165	170	175	
Lys	Leu	Ile	Leu	Lys	Arg	Gln	Val	Cys	Asn	Glu	Ile	Asn	Thr	Ile	Ser	180	185	190	
Asn	Ile	Met	Ala	Asp	Phe	Val	Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	195	200	205	
Asp	Gly	Asp	Ile	Gly	Val	Asp	Ile	Ser	Val	Thr	Gly	Ala	Pro	Val	Ile	210	215	220	
Thr	Ala	Thr	Tyr	Leu	Glu	Ser	His	His	Lys	Gly	His	Phe	Thr	His	Lys	225	230	235	240
Asn	Val	Ser	Glu	Ala	Phe	Pro	Leu	Arg	Ala	Phe	Pro	Pro	Gly	Leu	Leu	245	250	255	

001630 016300

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn  
260 265 270  
Ser Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu  
275 280 285  
Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr  
290 295 300  
Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln  
305 310 315 320  
Ala Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln  
325 330 335  
Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe  
340 345 350  
Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp  
355 360 365  
Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu  
370 375 380  
His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser  
385 390 395 400  
Ser Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser  
405 410 415  
Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser  
420 425 430  
Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val  
435 440 445  
Ala Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile  
450 455 460  
Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met  
465 470 475 480  
Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu  
485 490 495  
Ser

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Nagashima, Mariko  
McLean, John W.  
Lawn, Richard M.
- (B) TITLE: Cloning and mRNA tissue distribution of  
rabbit cholesteryl ester transfer protein
- (C) JOURNAL: J. Lipid Res.

00110001010000

(xi) SEQUENCE DESCRIPTION: SEO ID NO:27:

GCCTGTCCCA	AAGGCGCCTC	CTACGAGGCT	GGCATCGTGT	GTGCGATCAC	CAAGCCC GCC	60
CTCTTGGTGT	TGAACCAAGA	GACGGCCAAG	GTGGTCCAGA	CGGCCTTCCA	GCGCGCCGGC	120
TATCCGGACG	TCAGCGGCGA	GAGGGCCGTG	ATGCTCCTCG	GCCGGGTCAA	GTACGGGCTG	180
CACAACCTCC	AGATCAGCCA	CCTGTCCATC	GCCAGCAGCC	AGGTGGAGCT	GGTGGACGCC	240
AAGACCATCG	ACGTCGCCAT	CCAGAACGTG	TCCGTGGTCT	TCAAGGGGAC	CCTGAACTAC	300
AGCTACACGA	GTGCCTGGGG	GTGGGCATC	AATCAGTCTG	TCGACTTCGA	GATCGACTCT	360
GCCATTGACC	TCCAGATCAA	CACAGAGCTG	ACCTGCGACG	CTGGCAGTGT	GCGCACCAAT	420
GCCCCGACT	GCTACCTGGC	TTCCATAAA	CTGCTCCTGC	ACCTCCAGGG	GGAGCGCGAG	480
CCGGGGTGGC	TCAAGCAGCT	CTTCACAAAC	TTCATCTCCT	TCACCCTGAA	GCTGATTCTG	540
AAGCGACAGG	TCTGCAATGA	GATCAACACC	ATCTCCAACA	TCATGGCTGA	CTTTGTCCAG	600
ACGAGGGCCG	CCAGCATCCT	CTCAGATGGA	GACATCGGGG	TGGACATTTC	CGTGACGGGG	660
GCCCCTGTCA	TCACAGCCAC	CTACCTGGAG	TCCCATCACA	AGGGTCACTT	CACGCACAAG	720
AACGTCTCCG	AGGCCTTCCC	CCTCCGCGCC	TTCCCGCCCG	GTCTTCTGGG	GGACTCCCGC	780
ATGCTCTACT	TCTGGTTCTC	CGATCAAGTG	CTCAACTCCC	TGGCCAGGGC	CGCCTTCCAG	840
GAGGGCCGTC	TCGTGCTCAG	CCTGACAGGG	GATGAGTTCA	AGAAAGTGCT	GGAGACCCAG	900
GGTTTCGACA	CCAACCAGGA	AATCTTCCAG	GAGCTTTCCA	GAGGCCTTCC	CACCGGCCAG	960
GCCCAGGTAG	CCGTCCACTG	CCTTAAGGTG	CCCAAGATCT	CCTGCCAGAA	CCGGGGTGTC	1020
GTGGTGTCTT	CTTCCGTCGC	CGTGACGTTT	CGCTTCCCCC	GCCCAGATGG	CCGAGAAGCT	1080
GTGGCCTACA	GGTTTGAGGA	GGATATCATC	ACCACCGTCC	AGGCCTCCTA	CTCCCAGAAA	1140
AAGCTCTTCC	TACACCTCTT	GGATTTCAG	TGCGTGCCGG	CCAGCGGAAG	GGCAGGCAGC	1200
TCAGCAAATC	TCTCCGTGGC	CCTCAGGACT	GAGGCTAAGG	CTGTTTCCAA	CCTGACTGAG	1260
AGCCGCTCCG	AGTCCCTGCA	GAGCTCTCTC	CGCTCCCTGA	TCGCCACGGT	GGGCATCCCG	1320
GAGGTCATGT	CTCGGCTCGA	GGTGGCGTTC	ACAGCCCTCA	TGAACAGCAA	AGGCCTGGAC	1380
CTCTTCGAAA	TCATCAACCC	CGAGATTATC	ACTCTCGATG	GCTGCCTGCT	GCTGCAGATG	1440
GACTTCGGTT	TTCCCAAGCA	CCTGCTGGTG	GATTTCTGTC	AGAGCCTGAG	CTAG	1494

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Drayna, Dennis  
Jarnagin, Alisha Stephens  
McLean, John  
Henzel, William  
Kohr, William  
Fielding, Christopher  
Lawn, Richard

(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer protein cDNA

(C) JOURNAL: Nature

(D) VOLUME: 327

(F) PAGES: 632-634

(G) DATE: June 18-1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys 1	Ser	Lys	Gly	Thr 5	Ser	His	Glu	Ala	Gly 10	Ile	Val	Cys	Arg	Ile 15	Thr
Lys	Pro	Ala	Leu 20	Leu	Val	Leu	Asn	His 25	Glu	Thr	Ala	Lys	Val 30	Ile	Gln
Thr	Ala	Phe 35	Gln	Arg	Ala	Ser	Tyr 40	Pro	Asp	Ile	Thr	Gly 45	Glu	Lys	Ala
Met	Met 50	Leu	Leu	Gly	Gln	Val 55	Lys	Tyr	Gly	Leu	His 60	Asn	Ile	Gln	Ile
Ser 65	His	Leu	Ser	Ile	Ala 70	Ser	Ser	Gln	Val	Glu 75	Leu	Val	Glu	Ala	Lys 80
Ser	Ile	Asp	Val	Ser 85	Ile	Gln	Asn	Val	Ser 90	Val	Val	Phe	Lys	Gly 95	Thr
Leu	Lys	Tyr	Gly 100	Tyr	Thr	Thr	Ala	Trp 105	Trp	Leu	Gly	Ile	Asp 110	Gln	Ser
Ile	Asp	Phe 115	Glu	Ile	Asp	Ser	Ala 120	Ile	Asp	Leu	Gln	Ile 125	Asn	Thr	Gln
Leu	Thr 130	Cys	Asp	Ser	Gly	Arg 135	Val	Arg	Thr	Asp	Ala 140	Pro	Asp	Cys	Tyr
Leu 145	Ser	Phe	His	Lys	Leu 150	Leu	Leu	His	Leu	Gln 155	Gly	Glu	Arg	Glu	Pro 160
Gly	Trp	Ile	Lys	Gln 165	Leu	Phe	Thr	Asn	Phe 170	Ile	Ser	Phe	Thr	Leu 175	Lys
Leu	Val	Leu	Lys 180	Gly	Gln	Ile	Cys	Lys 185	Glu	Ile	Asn	Val	Ile 190	Ser	Asn
Ile	Met	Ala 195	Asp	Phe	Val	Gln	Thr 200	Arg	Ala	Ala	Ser	Ile 205	Leu	Ser	Asp
Gly	Asp 210	Ile	Gly	Val	Asp	Ile 215	Ser	Leu	Thr	Gly	Asp 220	Pro	Val	Ile	Thr
Ala 225	Ser	Tyr	Leu	Glu	Ser 230	His	His	Lys	Gly	His 235	Phe	Ile	Tyr	Lys	Asn 240
Val	Ser	Glu	Asp	Leu 245	Pro	Leu	Pro	Thr	Phe 250	Ser	Pro	Thr	Leu	Leu 255	Gly
Asp	Ser	Arg 260	Met	Leu	Tyr	Phe	Trp	Phe 265	Ser	Glu	Arg	Val	Phe 270	His	Ser
Leu	Ala 275	Lys	Val	Ala	Phe	Gln	Asp 280	Gly	Arg	Leu	Met	Leu 285	Ser	Leu	Met

Gly	Asp	Glu	Phe	Lys	Ala	Val	Leu	Glu	Thr	Trp	Gly	Phe	Asn	Thr	Asn
290						295					300				
Gln	Glu	Ile	Phe	Gln	Glu	Val	Val	Gly	Gly	Phe	Pro	Ser	Gln	Ala	Gln
305					310					315					320
Val	Thr	Val	His	Cys	Leu	Lys	Met	Pro	Lys	Ile	Ser	Cys	Gln	Asn	Lys
				325					330					335	
Gly	Val	Val	Val	Asn	Ser	Ser	Val	Met	Val	Lys	Phe	Leu	Phe	Pro	Arg
			340					345					350		
Pro	Asp	Gln	Gln	His	Ser	Val	Ala	Tyr	Tyr	Phe	Glu	Glu	Asp	Ile	Val
		355					360					365			
Thr	Thr	Val	Gln	Ala	Ser	Tyr	Ser	Lys	Lys	Lys	Leu	Phe	Leu	Ser	Leu
	370					375					380				
Leu	Asp	Phe	Gln	Ile	Thr	Pro	Lys	Thr	Val	Ser	Asn	Leu	Thr	Glu	Ser
385					390					395					400
Ser	Ser	Glu	Ser	Ile	Gln	Ser	Phe	Leu	Gln	Ser	Met	Ile	Thr	Ala	Val
				405					410					415	
Gly	Ile	Pro	Glu	Val	Met	Ser	Arg	Leu	Glu	Val	Val	Phe	Thr	Ala	Leu
			420					425					430		
Met	Asn	Ser	Lys	Gly	Val	Ser	Leu	Phe	Asp	Ile	Ile	Asn	Pro	Glu	Ile
		435					440					445			
Ile	Thr	Arg	Asp	Gly	Phe	Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro
	450					455					460				
Glu	His	Leu	Leu	Val	Asp	Phe	Leu	Gln	Ser	Leu	Ser				
465					470					475					

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Swenson, T. L.  
et al.,
- (C) JOURNAL: J. Biol. Chem.
- (D) VOLUME: 264
- (F) PAGES: 14318-14326
- (G) DATE: 1989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Arg	Asp	Gly	Phe	Leu	Leu	Leu	Gln	Met	Asp	Phe	Gly	Phe	Pro	Glu	His
1				5					10					15	
Leu	Leu	Val	Asp	Phe	Leu	Gln	Ser	Leu	Ser						
		20						25							

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 493 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(A) AUTHORS: Pape, Michael E.

Marotti, Keith R.

Melchior, George W

Molecular Cloning, S

(C) JOURNAL: Arteriosclerosis and Thrombosis

(D) VOLUME: 11

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Met 1	Leu	Ala	Ala	Thr 5	Val	Leu	Thr	Leu	Ala 10	Leu	Leu	Gly	Asn	Val 15	His
Ala	Cys	Ser	Lys 20	Gly	Thr	Ser	His	Lys 25	Ala	Gly	Ile	Val	Cys 30	Arg	Ile
Thr	Lys	Pro 35	Ala	Leu	Leu	Val	Leu 40	Asn	Gln	Glu	Thr	Ala 45	Lys	Val	Ile
Gln	Ser 50	Ala	Phe	Gln	Arg	Ala 55	Asn	Tyr	Pro	Asn	Ile 60	Thr	Gly	Glu	Lys
Ala 65	Met	Met	Leu	Leu	Gly 70	Gln	Val	Lys	Tyr	Gly 75	Leu	His	Asn	Ile	Gln 80
Ile	Ser	His	Leu	Ser 85	Ile	Ala	Ser	Ser	Arg 90	Val	Glu	Leu	Val	Glu	Ala 95
Lys	Ser	Ile	Asp 100	Val	Ser	Ile	Gln	Asn 105	Val	Ser	Val	Val	Phe	Lys	Gly
Thr	Leu	Lys 115	Tyr	Gly	Tyr	Thr	Thr 120	Ala	Trp	Gly	Leu	Gly 125	Ile	Asp	Gln
Ser	Val 130	Asp	Phe	Glu	Ile	Asp 135	Ser	Ala	Ile	Asp	Leu 140	Gln	Ile	Asn	Thr
Gln 145	Leu	Thr	Cys	Asp	Ser 150	Gly	Arg	Val	Arg	Thr 155	Asp	Ala	Pro	Asp	Cys 160
Tyr	Leu	Ser	Phe	His 165	Lys	Leu	Leu	Leu	His 170	Leu	Gln	Gly	Glu	Arg 175	Glu
Pro	Gly	Trp	Ile 180	Lys	Gln	Leu	Phe	Thr 185	Asn	Phe	Ile	Ser	Phe	Thr	Leu
Lys	Leu	Val 195	Leu	Lys	Gly	Gln	Ile 200	Cys	Lys	Glu	Ile	Asn 205	Ile	Ile	Ser
Asn	Ile 210	Met	Ala	Asp	Phe	Val 215	Gln	Thr	Arg	Ala	Ala 220	Ser	Ile	Leu	Ser
Asp 225	Gly	Asp	Ile	Gly	Val 230	Asp	Ile	Ser	Leu	Thr 235	Gly	Asp	Pro	Ile	Ile 240
Thr	Ala	Ser	Tyr	Leu 245	Glu	Ser	His	His	Lys 250	Gly	Tyr	Phe	Ile	Tyr 255	Lys

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGGCTG CCACCGTCCT GACCCTGGCC CTGCTGGGCA ATGTCCACGC CTGCTCCAAA	60
GGTACCTCAC ACAAGGCAGG CATTGTGTGC CGCATCACCA AGCCTGCCCT CCTGGTGTG	120
AACCAACAGA CTGCCAAGGT GATCCAGTCT GCCTTCCAGC GAGCCAACTA CCCAAATATC	180
ACAGGCGAGA AGGCCATGAT GCTCCTTGGC CAAGTCAAGT ATGGGTTGCA CAACATCCAA	240
ATCAGCCACT TGTCCATCGC CAGCAGCCGG GTGGAGCTGG TGAAGCCAA GTCCATTGAT	300
GTCTCCATTG AGAACGTGTC TGTGGTCTTC AAGGGGACCC TGAAGTATGG CTACACCACT	360
GCCTGGGGGC TGGGCATTGA TCAGTCCGTT GACTTCGAGA TCGACTCTGC CATTGACCTC	420
CAGATCAACA CACAACCTGAC CTGTGACTCT GGTTAGAGTGA GGACTGATGC CCCTGACTGC	480
TACCTGTCTT TCCATAAGCT GCTCCTGCA TCCCAAGGGG AGCGAGAGCC CGGGTGGATC	540
AAGCAGCTGT TCACAACTT CATCTCCTTC ACCCTGAAGC TGGTCCTGAA GGGACAGATC	600
TGCAAGAGA TCAACATCAT CTCCAACATC ATGGCCGATT TTGTCCAGAC AAGGGCTGCC	660
AGTATCCTTT CAGATGGAGA CATCGGGGTG GACATTTCCC TGACAGGTGA TCCCATCATT	720
ACAGCCTCCT ACCTGGAGTC CCATCACAA GGTATTATTC TCTATAAGAA TGTCTCGGAG	780
GACCTCCCAC TCCCCACCTT CTCGCCCGCA CTGCTGGGGG ACTCCCGCAT GCTGTACTTC	840
TGGTTCTCCG AGCAAGTCTT CCACTCCCTG GCCAAGGTAG CTTTCCAAGA TGCCCGCCTC	900
ACGCTCAGCC TGATGGGAGA CGAGTTCAAG GCAGTGCTGG AGACCTGGGG CTTCAACACC	960
AACCAAGAAA TCTTCCAGGA GGTTGTCGGC GGCTTCCCCA GCCAGGCCCA AGTCACCGTC	1020
CACTGCCTCA AGATGCCCAG GATCTCCTGC CAAAACAAGG GAGTCGTGGT CAATTCTTCG	1080
GTGATGGTGA AATTCCTCTT TCCACGCCCA GACCAGCAAC ACTCTGTAGC TTACACATTT	1140
GAAGAGGATA TCATGACCAC CGTCCAGGCC TCCTATTCTA AGAAAAAGCT CTTCTTAAGC	1200
CTCTTGGA TTCCAGATTAC ACCAAAGACT GTTCCAAC TGAAGTGAAG CAGCTCCGAG	1260
TCCGTCCAGA GCTTCCTGCA GTCAATGATC ACCACTGTGG GCATCCCTGA GGTCATGTCT	1320
CGGCTTGAGG CAGTGTTTAC AGCCCTCATG AACAGCAAAG GCCTGAGCCT CTTGACATC	1380
ATCAATCCTG AGATTATCAC TCGAGATGGC TTCCTGCTGC TGCAGATGGA CTTTGGCTTC	1440
CCTGAGCACC TGCTGGTGGA TTTCTCCAG AGCTTGAGCT AGAAGTCTCC AAGGACGTCA	1500
GGATGGGG	1508

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln  
1 5 10 15  
Val Thr Val His  
20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val  
1 5 10 15  
Ala Tyr Thr Phe  
20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp  
1 5 10 15  
Phe Leu Gln Ser Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu  
1 5 10 15  
Leu Asp Phe Gln  
20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln  
 1 5 10 15  
 Leu Phe Thr Asn  
 20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asn Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr  
 1 5 10 15  
 Gly Leu His Asn  
 20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:39:

(A) LENGTH: 552 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(2) INFORMATION FOR SEQ ID NO:40:

(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val  
1 5 10 15

Val Ser Tyr Val Asn Thr Asn Met Gly  
20 25

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

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Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
1          5          10          15

Ile Glu Tyr Leu Val
          20

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro  
1 5 10 15  
Asn Ala Pro Ile Leu  
20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCCATGG ACATCGACCC TTATAAGAA TTTGG

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT TTAACATTGA GATTCCCGAG ATTGAGATCT TCTG

44

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCGAATTC ACTAGTTGGA AGATCCAGCG TCTAGAGACC TAG

43

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATCGAATTC CTCGAGCTAG AGTCATTAGT TCCCCCAGC A

41

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs

(ii) MOLECULE TYPE: cDNA

GATTATCACT CGAGATGGCT TCCTGCTGCT GCAG

34

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

GATCGAATTC AGCGCTCAAG CTCTGGAGGA AATCCACCAG

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His  
1 5 10 15

Leu Leu Val Asp Phe Leu Gln Ser Leu Ser  
20 25